

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 4, 2005, 12:01:00 ; Search time 13047 Seconds  
(without alignments)  
1.752 Million cell updates/sec

Title: US-09-982-091A-5

Perfect score: 58837

Sequence: 1 aagcagtagtttaactt.....tatgccagcagttccctgag 58837

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 1 segs, 194296 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : al354864.gb\_pr:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	58837	100.0	194296	1	AL354864	ACCESSION:AL354864
2	558.173	0.9	194296	1	AL354864	ACCESSION:AL354864

ALIGNMENTS

RESULT 1  
AL354864 194296 bp DNA linear PRI 04-APR-2001  
LOCUS Human DNA sequence from clone RPI1-435D7 on chromosome 1. Contains  
DEFINITION ESTs, STSs, GSSs and Cpg Islands. Contains a novel gene and the 5'  
part of the PSMB2 gene for proteasome (prosome, macropain) subunit  
2, beta type, complete sequence.  
AL354864  
AL354864.16 GI:10185566  
HTG, Cpg Island, macropain, prosome, proteasome, PSMB2.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 194296)  
AUTHORS Howden, P.  
TITLE Direct Submission  
JOURNAL Submitted (06-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone  
requests: clonerequest@sanger.ac.uk  
On Sep 19, 2000 this sequence version replaced gi:9714820.  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variation annotation may not be found in the sequence submission  
corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.  
The following abbreviations are used to associate primary accession  
numbers given in the feature table with their source databases:  
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information  
on the WORMPEP database can be found at  
http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence  
was generated from part of bacterial clone contigs of human  
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping  
Group. Further information can be found at  
http://www.sanger.ac.uk/HGP/Chr1  
This sequence is the entire insert of clone RPI1-435D7 The true  
left end of clone RPI1-62B3 is at 123829 in this sequence. The true  
right end of clone RPI1-555P23 is at 81044 in this sequence. This  
sequence has been finished according to sequence map criteria as  
follows. An attempt is made to resolve all sequencing problems,  
such as compressions and repeats, but not necessarily within known  
annotated repeat sequence elements. Where the sequence is  
ambiguous, there is an annotation using the 'unsure' feature key.  
RPI1-435D7 is from the library RPI1-11.2 constructed by the group  
of Pieter de Jong. For further details see  
http://www.chori.org/bacpac/home.htm  
VECTOR: pBACe3.6.

FEATURES

source

Location/Qualifiers  
1..194296  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="1"  
/clone="RPI1-435D7"  
/clone\_1b="RPI1-11.2"  
72..131  
/note="15 copies 4 mer cctt 78% conserved"  
2010..2057  
/note="24 copies 2 mer tt 75% conserved"  
2353..2650  
/note="AluSg1 repeat: matches 1..301 of consensus"  
5390..6351  
/note="Cpg island"  
/evidence=not\_experimental  
7263..7656  
/note="MLT1B repeat: matches 1..390 of consensus"  
8017..8605  
/note="Cpg island"  
/evidence=not\_experimental  
11677..12004  
/note="LIMB6 repeat: matches 5474..5827 of consensus"  
12328..12620  
/note="LIMB6 repeat: matches 5188..5474 of consensus"  
12659..13001  
/note="LIMB6 repeat: matches 4844..5199 of consensus"  
13304..13326  
/note="LIMB6 repeat: matches 4822..4844 of consensus"  
13627..13881  
/note="LIMB6 repeat: matches 4601..4822 of consensus"  
13883..13938  
/note="28 copies 2 mer tg 96% conserved"  
14265..14436  
/note="LIMB6 repeat: matches 4442..4609 of consensus"  
14734..14909  
/note="LIMB6 repeat: matches 4265..4442 of consensus"  
14919..14956  
/note="LIMB6 repeat: matches 1..38 of consensus"  
14957..14986  
/note="LIMB6 repeat: matches 4243..4276 of consensus"  
15300..15341  
/note="LIMB6 repeat: matches 4197..4243 of consensus"  
15639..16080  
/note="LIP8 repeat: matches 5714..6155 of consensus"  
16081..16208  
/note="LIMB6 repeat: matches 4103..4197 of consensus"  
17572..17808  
/note="MLT1G repeat: matches 3..221 of consensus"  
18105..18136